

GenCore Version 5.1.6
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OM protein - protein search, using sw/model

Run on: June 25, 2003, 14:40:41 ; Search time 12.6202 Seconds
(without alignments)
837.928 Million cell updates/sec

Title: US-09-622-613b-15

Perfect score: 602

Sequence: 1 QNMTFOOKHIIINTPIICNT.....ICVKCENQYVHFAGIGRCP 110

Scoring table: BLDJSM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : FIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	588.5	97.8	111 2	A27121	ribonuclease-relat
2	455	75.6	111 1	JX0120	ribonuclease-relat
3	374	62.1	111 2	JX0085	pancreatic ribonuc
4	274.5	45.6	104 2	A39035	ribonuclease-relat
5	135.5	32.5	124 1	NRWHR	pancreatic ribonuc
6	135.5	32.5	145 1	A35932	angiogenin precurs
7	133.5	32.2	167 2	S20066	pancreatic-type ri
8	132.5	32.0	124 1	NRPG	pancreatic ribonuc
9	131.5	31.8	119 2	S41111	pancreatic ribonuc
10	122.5	30.3	124 1	NRPRH	pancreatic ribonuc
11	122	30.3	122 1	NRKGR	pancreatic ribonuc
12	120.5	30.0	128 1	NRUC	pancreatic ribonuc
13	120.5	30.0	149 1	NRMS	pancreatic ribonuc
14	119.5	29.9	123 1	A43825	angiogenin - pig
15	118.5	29.7	128 1	NRGPB	pancreatic ribonuc
16	117.5	29.5	128 1	NRHM	pancreatic ribonuc
17	116.5	29.4	124 1	NRCHM	pancreatic ribonuc
18	116.5	29.4	124 1	NRCHM	pancreatic ribonuc
19	116.5	29.4	124 1	NRCHM	pancreatic ribonuc
20	116.5	29.4	128 1	NRKS	pancreatic ribonuc
21	114.5	19.0	124 1	S08549	ribonuclease - dom
22	114	18.9	125 1	A32474	angiogenin (valida
23	113.5	18.9	124 1	NRHDE	pancreatic ribonuc
24	113	18.8	147 1	NRHDE	angiogenin precurs
25	112.5	18.7	124 1	NRGE	pancreatic ribonuc
26	112.5	18.7	124 1	NRDEO	pancreatic ribonuc
27	112	18.6	125 1	S43825	angiogenin - rabbi
28	111.5	18.5	130 2	S22808	pancreatic ribonuc
29	110.5	18.4	124 1	NRBOB	pancreatic ribonuc

30	110.5	18.4	124 1	NRMB	pancreatic ribonuc
31	110.5	18.4	124 1	NREKN	pancreatic ribonuc
32	110.5	18.4	124 2	S07141	pancreatic ribonuc
33	110.5	18.4	124 2	JC5360	pancreatic ribonuc
34	110.5	18.4	150 1	NRBO	pancreatic ribonuc
35	110.5	18.4	158 2	161900	eosinophil-derived
36	109.5	18.2	124 1	NRSH	pancreatic ribonuc
37	108.5	18.0	119 2	JX0115	pancreatic ribonuc
38	108.5	18.0	124 1	NRGB	pancreatic ribonuc
39	108.5	18.0	132 1	NRRT	pancreatic ribonuc
40	106.5	17.7	124 1	NRHP	pancreatic ribonuc
41	106.5	17.7	125 4	A47498	pancreatic ribonuc
42	106.5	17.7	150 1	NRBOS	seminal ribonuclea
43	104.5	17.4	124 1	NRGN	pancreatic ribonuc
44	104.5	17.4	124 1	NRDEF	pancreatic ribonuc
45	104	17.3	125 2	S04503	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121 ribonuclease-related stalic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993

C:Accession: A27121

R:Tilani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayan

Biochemistry 26, 2189-2194, 1987.

A:Title: Amino acid sequence of stalic acid-binding lectin from frog (Rana catesbeiana

A:Reference number: A27121; MUID:87299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <TTP>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match 97.8%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 1.4e-51;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 QNMTFOOKHIIINTPII-CNTIMDNIIYVGGCKRVNTFLISSATVKAICTGVIMNV 59
Db 1 ENMTFOOKHIIINTPII-CNTIMDNIIYVGGCKRVNTFLISSATVKAICTGVIMNV 60

QY 60 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVCKENQYVHFAGIGRCP 110
Db 61 LSTRFOLNCTRTSITPRPCPYSSRTETNYICVCKENQYVHFAGIGRCP 111

RESULT 2

JX0120 ribonuclease-related stalic acid-binding lectin - Japanese frog

C:Species: Rana japonica (Japanese frog)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JX0120

R:Kamita, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayana

J. Biochem. 108, 139-143, 1990

A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.

A:Reference number: JX0120; MUID:91035319; PMID:2229005

A:Accession: JX0120

A:Molecule type: protein

A:Residues: 1-111 <KAM>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin; pyroglyutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:19-72,34-82,52-97,94-111/Dissulfide bonds: #status experimental

Query Match 75.6%; Score 455; DB 1; Length 111;
Best Local Similarity 76.4%; Pred. No. 2.6e-38;
Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

Db 6 AKFERQIHDSNPSSSSNNYCNOMKSR-NLTGCRCKPVNTFVHESLADYQAVCS---QK 61
 QY 58 NVL-----STTRPOLNTCTRTSITPRP-CPYSSRTETNYCKCE-NQY-PVHF 103
 Db 62 NVACKNQITNCYQSYSTMSITDCKETGSSKPKNCAYKTKQAKKHIIIVACEGPNVPVHF 120

RESULT 11

NRKCR

pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
 N:Alternate names: RNase 1; RNase A
 C:Species: Macropus rufus, Megaleia rufa (red kangaroo)
 C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
 C:Accession: A00833
 R:Gastrin, W.; Wellington, G.W.; Belintema, J.J.
 E: Eur. J. Biochem. 86, 209-217, 1978
 A:Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
 A:Reference number: A00833; MUID:78190621; PMID:658039
 A:Accession: A00833
 A:Molecule type: protein
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:11-40/117/Active site: His, Lys, His #status predicted
 F:25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
 F:61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 20.3%; Score 122; DB 1; Length 122;
 Best Local Similarity 30.7%; Pred. No. 3.6e-05;
 Matches 35; Conservative 16; Mismatches 45; Indels 18; Gaps 6;

QY 6 FQOKHI-----INTPIICNTIMDNINIIYVGQCKRVNFIISATYKAI-----51
 Db 7 FORQHMDSHSTYSSNNYCNLMKKAR-DMTSGCKRLNFIHPRKSVDAVCHQENVTK 65
 QY 52 TGVNNNVSTTRFQOLNTCTRTSITPRP-CPYSSRTETNYCKCE-NQY-PVHF 103
 Db 66 NQRTNC-YKSNRSLSTTNCROTGASKYPCQYETSMLNQTIIIVACEGQYVPVHF 118

RESULT 12

NRUCU

pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
 N:Alternate names: RNase 1; RNase A
 C:Species: Myocastor coypus (nutria, coypu)
 C>Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
 C:Accession: A00822
 R:van den Berg, A.; van den Hende-Timmer, L.; Belintema, J.J.
 Biochim. Biophys. Acta 453, 400-409, 1976
 A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
 A:Reference number: A90612; MUID:77065676; PMID:999896
 A:Accession: A00822
 A:Molecule type: protein
 A:Residues: 1-128 <VAN>

C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12,41,119/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 20.0%; Score 120.5; DB 1; Length 128;
 Best Local Similarity 31.6%; Pred. No. 5.4e-05;
 Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;

QY 6 FQOKHI-----INTPIICNTIMDNINIIYVGQCKRVNFIISATYKAICTGYINNV 59
 Db 8 FERQHMDSRGSPSTNPNYCNEMKSR-NMTGCRCKPVNTFVHESLADYQAVC---FQKNV 63
 QY 60 L-----STTRFQOLNTCTRTSITPRP-CPYSSRTETNYCKCE-NQY-PVHF 103
 Db 64 LCKNGQITNCYQSNMHTTDCRVTNSDYPNCSTRTSOEKSIVACEGPNVPVHF 120

RESULT 13

NRMS

pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
 N:Alternate names: RNase 1; RNase A
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
 C:Accession: A34090; S22598; A00830
 R:Schueller, C.; Nijssen, H.M.J.; Kok, R.; Belintema, J.J.
 Mol. Biol. Evol. 7, 29-44, 1990
 A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mo
 A:Reference number: A34090; MUID:90136034; PMID:2299980
 A:Accession: A34090
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-149 <SCCH>

A:Cross-references: GB:M27814; NID:q200762; PIDN:AAA40060.1; PID:q200763
 R:Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koepf, D.; Meister, M.H.
 Nucleic Acids Res. 19, 6935-6941, 1991
 A:Title: Isolation of the murine ribonuclease gene Rb-1: structure and tissue specific
 A:Reference number: S22598; MUID:92107684; PMID:1840677
 A:Accession: S22598
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-149 <SAM>

A:Cross-references: EMBL:X60103; NID:q53981; PIDN:CAA42697.1; PID:q53982
 R:Leustra, J.A.; Belintema, J.J.
 Eur. J. Biochem. 98, 399-408, 1979
 A:Title: The amino acid sequence of mouse pancreatic ribonuclease.
 A:Reference number: A00830; MUID:80024269; PMID:556267
 A:Accession: A00830
 A:Molecule type: protein
 A:Residues: 26-149 <LEN>

C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-149/Product: pancreatic ribonuclease #status experimental <MAT>
 F:137-66,144/Active site: His, Lys, His #status predicted
 F:51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
 F:62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.0%; Score 120.5; DB 1; Length 149;
 Best Local Similarity 30.8%; Pred. No. 6.3e-05;
 Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

QY 6 FQOKHI-----INTPIICNTIMDNINIIYVGQCKRVNFIISATYKAICTGYINNV 59
 Db 33 FORQHMDSHSTYSSNNYCNLMKKAR-DMTNSCKRPNVTFVHESLADYQAVCS---QENV 88
 QY 60 L-----STTRFQOLNTCTRTSITPRP-CPYSSRTETNYCKCE-NQY-PVHF 103
 Db 89 TCKNRKSNCKYSSALHTTDCRLKNSKYPNCQYKTKTQYQKHIIIVACEGPNVPVHF 145

RESULT 14

AA3825

angiotensin - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S29834; A43825
 R:Bond, M.D.; Strydom, D.J.; Vallée, B.L.
 Biochim. Biophys. Acta 1162, 177-186, 1993
 A:Title: Characterization and sequencing of rabbit, pig and mouse angiotensins: discer
 A:Reference number: S29833; MUID:93192291; PMID:8448182
 A:Accession: S29834
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-123 <BOX>
 A>Note: this sequence was submitted to the Protein Sequence Database, December 1992
 C:Superfamily: pancreatic ribonuclease

Query Match 19.9%; Score 119.5; DB 1; Length 123;
 Best Local Similarity 39.5%; Pred. No. 6.5e-05;
 Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;

```

QY      33 CKRVNTEFISSATVKAICTG-----VINMNVLTTRFOLNCTRTSIPR-PCPYSSRTE 87
      11 ||||| : ||||| : ||| : ||| :
Db      39 CKRVNTEFIHGRNDIKKAIKCNKNGEPNFRSRKSPFOITCKKHGGSNRPCCGRATAG 98
      11 ||||| : ||||| : ||| : ||| :
QY      88 TNYICVKCENQYPVHF 103
      11 ||||| : ||||| : ||| : ||| :
Db      99 FRTIIVACENGLPVHF 114
      11 ||||| : ||||| : ||| : ||| :

```

RESULT 15

NRGPR

pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)

N:Alternate names: RNase IB

C:Species: Cavia porcellus (guinea pig)

C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000

C:Accession: A00826

R:van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J.

Eur. J. Biochem. 75, 91-100, 1977

A:Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure &

A:Reference number: A91247; MUID:77185023; PMID:862624

A:Accession: A00826

A:Molecule type: Protein

A:Residues: 1-128 <VAN>

A:Note: 64-Pro was also found

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12.41.119/Active site: His, Lys, His #status predicted

F:21.34/Binding site: carbonyl (Asn) (covalent) #status experimental

F:26.84.40-95.58-110.65-72/Disulfide bonds: #status predicted

Query Match 19.7%; Score 118.5; DB 1; Length 128;

Best Local Similarity 31.6%; Pred. No. 8.5e-05;

Matches 37; Conservative 14; Mismatches 43; Indels 23; Gaps 6;

```

QY      6 FQGH-----INPPICTIMDNMIYIVGGCKRVNTEFISSATVKAICTGVINNV 59
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      8 FORQHMDEGSPNSNSNCHVMIR-NMTGRCRPVNTFVHESLADVOAVC---FQKNV 63
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      60 L-----STRFOLNCTRTSIPR-PCPYSSRTEYICVKCENQ--YYPVHF 103
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      64 LCKNGQINCYOSYRMRTIDCRVTSSSKFPCNSTYRMSQAKSLIIVACEGDPYVPVHF 120
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Search completed: June 25, 2003, 14:58:04
 Job time : 12.6203 secs

